## CLAIMS LISTING

1. (Currently Amended)  A method of analyzing gene expressions comprising acts of:

    determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

    forming a first spatial-expression pattern by:

        selecting a chromosomal region having ~~a length and~~ an exon ~~having a start and a stop position~~; and

        associating the gene expression within the first gene expression pattern with its corresponding exon ~~by:~~

        ~~determining, within the chromosomal region, the start and stop position of the exon; and~~

        ~~associating the gene expression to the first-spatial expression pattern for the length between the start and stop position of the exon;~~ and

        <u>wherein the act of forming the first spatial-expression pattern further comprises an act of creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.</u>

2. (Cancelled)

3. (Currently Amended)  The method of claim <u>1</u> [[2]], wherein:

    the magnitude of the first spatial-expression pattern signal at points spanning the chromosomal region are a function of the expression level of an exon at corresponding positions in the chromosomal region.

4. (Currently Amended)  The method of claim <u>1</u> [[2]], further comprising an act of:

    identifying first regular spatial patterns in the first spatial-expression pattern signal.

5. (Withdrawn)  The method of claim 4, wherein

the act of identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

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6. (Withdrawn)  The method of claim 5, further comprising an act of:

identifying a group of genes contributing to local maximum points of the generated Fourier transform spectrum.

10    7. (Original)  The method of claim 4, wherein

the act of identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

8. (Original)  The method of claim 7, further comprising an act of:

15    identifying a group of genes contributing to local maximum points of the generated Wavelet transformed signal at different scales and positions.

9. (Original)  The method of claim 4, wherein:

the act of identifying first regular spatial patterns in the first spatial-expression

20    pattern signal identifies a set of genes.

10. (Original)  The method of claim 9, wherein:

the act of identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes which participate in a common biological process

25    or function.

11. (Original)  The method of claim 1, further comprising acts of:

determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and

forming a second spatial-expression pattern by:

selecting a chromosomal region having an exon; and

associating a gene expression within the second gene expression pattern

with its corresponding exon.

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12. (Original)  The method of claim 11, further comprising acts of:

identifying first regular spatial patterns in the first spatial-expression pattern

signal;

identifying second regular spatial patterns in the second spatial-expression pattern

10     signal; and

comparing the first and second regular spatial patterns.

13. (Original)  The method of claim 11, further comprising an act of:

repeating the steps of determining a gene expression pattern and forming a

15     spatial-expression pattern signal for any number of gene expression patterns.

14. (Original)  The method of claim 13, further comprising acts of:

comparing all formed spatial-expression pattern signals.

20     15. (Original)  The method of claim 14, wherein:

the act of comparing all formed spatial-expression pattern signals  involves

clustering all formed spatial-expression pattern signals.

16. (Original)  The method of claim 15, further comprising acts of:

25     identifying gene groups contributing to the differences in significant changes in

the first and second regular spatial-expression pattern signals.

17. (Original)  The method of claim 1, wherein the chromosomal region is an entire

chromosome.

18. (Original) The method of claim 11, wherein:

        the first spatial-expression pattern and the second-expression pattern are selected from different chromosomes.

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19. (Original) The method of claim 11, wherein:

        the first  spatial-expression and the second-expression pattern are selected from different genomes.

10   20. (Currently Amended)  An apparatus for analyzing gene expressions, the apparatus comprising a computer system including a processor, a memory coupled with the processor, an input coupled with the processor for receiving input data, and an output coupled with the processor for outputting data, wherein the computer system further comprises means, residing in its processor and memory, for:

15          determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

        forming a first spatial-expression pattern by:

                selecting a chromosomal region having a length and an exon having a start and a stop position; and

20          associating the gene expression within the first gene expression pattern with its corresponding exon by:

                determining, within the chromosomal region, the start and stop position of the exon; and

                associating the gene expression to the first-spatial expression pattern for

25          the length between the start and stop position of the exon; and

                wherein the means for forming the first spatial-expression pattern further comprises means for creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-

expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

21. (Cancelled)

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22. (Currently Amended)  An apparatus as set forth in claim 20 [[21]], wherein:

      the magnitude of the first spatial-expression pattern signal at points spanning the chromosomal region are a function of the expression level of an exon at corresponding positions in the chromosomal region.

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23. (Currently Amended)  An apparatus as set forth in claim 20 [[21]], further comprising an means for:

      identifying first regular spatial patterns in the first spatial-expression pattern signal.

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24. (Withdrawn)  An apparatus as set forth in claim 23, wherein

      the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

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25. (Withdrawn)  An apparatus as set forth in claim 24, further comprising an means for:

      identifying a group of genes contributing to local maximum points of the generated Fourier transform spectrum.

25    26. (Original)  An apparatus as set forth in claim 23, wherein

      the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

27. (Original)  An apparatus as set forth in claim 26, further comprising an means for:

      identifying a group of genes contributing to local maximum points of the generated Wavelet transformed signal at different scales and positions.

5    28. (Original)  An apparatus as set forth in claim 23, wherein:

      the means for identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes.

29. (Original)  An apparatus as set forth in claim 28, wherein:

10      the means for identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes which participate in a common biological process or function.

30. (Original)  An apparatus as set forth in claim 20, further comprising acts of:

15      determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and

      forming a second spatial-expression pattern by:

      selecting a chromosomal region having an exon; and

      associating a gene expression within the second gene expression

20      pattern with its corresponding exon.

31. (Original)  An apparatus as set forth in claim 30, further comprising acts of:

      identifying first regular spatial patterns in the first spatial-expression pattern signal;

25      identifying second regular spatial patterns in the second spatial-expression pattern signal; and

      comparing the first and second regular spatial patterns.

32. (Original)  An apparatus as set forth in claim 31, further comprising an means for:

repeating the steps of determining a gene expression pattern and forming a spatial-expression pattern signal for any number of gene expression patterns.

33. (Original) An apparatus as set forth in claim 30, further comprising acts of:

5              comparing all formed spatial-expression pattern signals.

34. (Original) An apparatus as set forth in claim 33, wherein:

the means for comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.

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35. (Original) An apparatus as set forth in claim 34 further comprising acts of:

identifying gene groups contributing to the differences in significant changes in the first and second regular spatial-expression pattern signals.

15   36. (Original) An apparatus as set forth in claim 20, wherein the chromosomal region is an entire chromosome.

37. (Previously Presented) An apparatus as set forth in claim 30, wherein:

the first spatial-expression pattern and the second-expression pattern are

20   selected from different chromosomes.

38. (Original) An apparatus as set forth in claim 30, wherein:

the first  spatial-expression and the second-expression pattern are selected from different genomes.

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39. (Currently Amended) A computer program product for analyzing gene expressions, the computer program product comprising means, encoded in a computer-readable medium for:

determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having ~~a length and~~ an exon ~~having a start~~

5        ~~and a stop position~~; and

associating the gene expression within the first gene expression pattern with its corresponding exon ~~by~~:

~~determining, within the chromosomal region, the start and stop position of~~

~~the exon; and~~

10        ~~associating the gene expression to the first-spatial expression pattern for~~

~~the length between the start and stop position of the exon~~; and

<u>wherein the means for forming the first spatial-expression pattern further</u>

<u>comprises means for creating a first spatial-expression pattern signal wherein the</u>

<u>first spatial-expression pattern signal is a representation of the first spatial-</u>

15        <u>expression pattern where a magnitude of the first spatial-expression pattern signal</u>

<u>at any point is determined by an expression level of the corresponding exon.</u>

40. (Cancelled)

20    41. (Currently Amended)  A computer program product as set forth in claim <u>39</u> [[40]], wherein:

the magnitude of the first spatial-expression pattern signal at points spanning the chromosomal region are a function of the expression level of an exon at corresponding positions in the chromosomal region.

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42. (Currently Amended)  A computer program product as set forth in claim <u>39</u> [[40]], further comprising an means for:

identifying first regular spatial patterns in the first spatial-expression pattern signal.

43. (Withdrawn)  A computer program product as set forth in claim 42, wherein

    the means for identifying first regular spatial patterns in the first spatial-

expression pattern signal is performed through the use of Fourier transform signal

5      processing.


44. (Withdrawn)  A computer program product as set forth in claim 43, further

    comprising an means for:

    identifying a group of genes contributing to local maximum points of the

10     generated Fourier transform spectrum.


45. (Original)  A computer program product as set forth in claim 42, wherein

    the means for identifying first regular spatial patterns in the first spatial-

expression pattern signal is performed through the use of Wavelet transform signal

15     processing.


46. (Original)  A computer program product as set forth in claim 45, further comprising

    an means for:

    identifying a group of genes contributing to local maximum points of the

20     generated Wavelet transformed signal at different scales and positions.


47. (Original)  A computer program product as set forth in claim 42, wherein:

    the means for identifying first regular spatial patterns in the first spatial-

expression pattern signal identifies a set of genes.

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48. (Original)  A computer program product as set forth in claim 47, wherein:

    the means for identifying first regular spatial patterns in the first spatial-

expression pattern signal identifies a set of genes which participate in a common

biological process or function.

49. (Original) A computer program product as set forth in claim 39, further comprising acts of:

    determining a second gene expression pattern for a second condition, wherein
5   the second gene expression pattern comprises a gene expression; and

        forming a second spatial-expression pattern by:

            selecting a chromosomal region having an exon; and

            associating a gene expression within the second gene expression pattern
        with its corresponding exon.

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50. (Original) A computer program product as set forth in claim 49, further comprising acts of:

    identifying first regular spatial patterns in the first spatial-expression pattern
    signal;

15       identifying second regular spatial patterns in the second spatial-expression
    pattern signal; and

        comparing the first and second regular spatial patterns.

51. (Original) A computer program product as set forth in claim 50, further comprising
20   an means for:

    repeating the steps of determining a gene expression pattern and forming a
    spatial-expression pattern signal for any number of gene expression patterns.

52. (Original) A computer program product as set forth in claim 49, further comprising
25   acts of:

    comparing all formed spatial-expression pattern signals.

53. (Original) A computer program product as set forth in claim 52, wherein:

the means for comparing all formed spatial-expression pattern signals

involves clustering all formed spatial-expression pattern signals.

54. (Original)  A computer program product as set forth in claim 53, further comprising

5        acts of:

identifying gene groups contributing to the differences in significant changes

in the first and second regular spatial-expression pattern signals.

55. (Previously Presented)  A computer program product as set forth in claim 39, wherein

10        the chromosomal region is an entire chromosome.

56. (Original)  A computer program product as set forth in claim 39, wherein:

the first spatial-expression pattern and the second-expression pattern are

selected from different chromosomes.

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57. (Original)  A computer program product as set forth in claim 39, wherein:

the first  spatial-expression and the second-expression pattern are selected

from different genomes.

20    58. (Currently Amended)  A method of analyzing gene expressions comprising acts of:

determining a first gene expression pattern for a first condition, wherein the

first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having a length and an exon having a start

25        and stop position;

associating the gene expression within the first gene expression pattern

with its corresponding exon by:

determining, within the chromosomal region, the start and stop

position of the exon; and

~~associating the gene expression to the first-spatial-expression~~

~~pattern for the length between the start and stop position of the exon;~~ and

creating a first spatial-expression pattern signal wherein the first spatial-

expression pattern signal is a representation of the first spatial-expression pattern

5          where a magnitude of the first spatial-expression pattern signal at any point is

determined by an expression level of the corresponding exon.


59. (Original)  The method of claim 58, further comprising an act of:

identifying first regular spatial patterns in the first spatial-expression pattern

10        signal.


60. (Withdrawn)  The method of claim 59, wherein

the act of identifying first regular spatial patterns in the first spatial-expression

pattern signal is performed through the use of Fourier transform signal processing.

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61. (Original)  The method of claim 59, wherein

the act of identifying first regular spatial patterns in the first spatial-expression

pattern signal is performed through the use of Wavelet transform signal processing.


20   62. (Original)  The method of claim 58, further comprising acts of:

determining a second gene expression pattern for a second condition, wherein

the second gene expression pattern comprises a gene expression; and

forming a second spatial-expression pattern by:

selecting a chromosomal region having an exon; and

25                associating a gene expression within the second gene expression pattern

with its corresponding exon.


63. (Original)  The method of claim 62, further comprising acts of:

identifying first regular spatial patterns in the first spatial-expression pattern signal;

identifying second regular spatial patterns in the second spatial-expression pattern signal; and

5          comparing the first and second regular spatial patterns.

64. (Original) The method of claim 62, further comprising acts of:

comparing all formed spatial-expression pattern signals.

10     65. (Original) The method of claim 64, wherein:

the act of comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.

66. (Currently Amended) An apparatus for analyzing gene expressions, the apparatus
15      comprising a computer system including a processor, a memory coupled with the processor, an input coupled with the processor for receiving input data, and an output coupled with the processor for outputting data, wherein the computer system further comprises means, residing in its processor and memory, for:

determining a first gene expression pattern for a first condition, wherein the
20      first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having ~~a length and~~ an exon ~~having a start and a stop position~~;

associating the gene expression within the first gene expression pattern
25      with its corresponding exon ~~by~~:

~~determining, within the chromosomal region, the start and stop position of the exon;~~

~~associating the gene expression to the first spatial expression~~
~~pattern for the length between the start and stop position of the exon~~; and

creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

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67. (Original) An apparatus as set forth in claim 66, further comprising an means for:

identifying first regular spatial patterns in the first spatial-expression pattern signal.

10    68. (Withdrawn) An apparatus as set forth in claim 67, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

15    69. (Original) An apparatus as set forth in claim 67, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

20    70. (Previously Presented) An apparatus as set forth in claim 66, further comprising acts of:

determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and

forming a second spatial-expression pattern by:

25          selecting a chromosomal region having an exon; and

associating a gene expression within the second gene expression pattern with its corresponding exon.

71. (Previously Presented)  An apparatus as set forth in claim 66, further comprising acts of:

       identifying first regular spatial patterns in the first spatial-expression pattern signal;

5       identifying second regular spatial patterns in the second spatial-expression pattern signal; and

       comparing the first and second regular spatial patterns.

72. (Previously Presented)  An apparatus as set forth in claim 66, further comprising acts

10     of:

       comparing all formed spatial-expression pattern signals.

73. (Previously Presented)  An apparatus as set forth in claim 72, wherein:

       the means for comparing all formed spatial-expression pattern signals

15    involves clustering all formed spatial-expression pattern signals.

74. (Currently Amended)  A computer program product for analyzing gene expressions, the computer program product comprising means, encoded in a computer-readable medium for:

20     determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

       forming a first spatial-expression pattern by:

           selecting a chromosomal region having a length and an exon having a start and a stop position;

25     associating the gene expression within the first gene expression pattern with its corresponding exon, by:

           determining, within the chromosomal region, the start and stop position of the exon; and

associating the gene expression to the first spatial expression
pattern for the length between the start and stop position of the exon; and
creating a first spatial-expression pattern signal wherein the first spatial-
expression pattern signal is a representation of the first spatial-expression pattern
5          where a magnitude of the first spatial-expression pattern signal at any point is
determined by an expression level of the corresponding exon.


75. (Original)  A computer program product as set forth in claim 74, further comprising
an means for:
10          identifying first regular spatial patterns in the first spatial-expression pattern
signal.


76. (Withdrawn)  A computer program product as set forth in claim 75, wherein
the means for identifying first regular spatial patterns in the first spatial-
15     expression pattern signal is performed through the use of Fourier transform signal
processing.


77. (Original)  A computer program product as set forth in claim 75, wherein
the means for identifying first regular spatial patterns in the first spatial-
20     expression pattern signal is performed through the use of Wavelet transform signal
processing.


78. (Original)  A computer program product as set forth in claim 74, further comprising
acts of:
25          determining a second gene expression pattern for a second condition, wherein
the second gene expression pattern comprises a gene expression; and
forming a second spatial-expression pattern by:
selecting a chromosomal region having an exon; and

associating a gene expression within the second gene expression pattern
with its corresponding exon.

79. (Original)  A computer program product as set forth in claim 78, further comprising

5       acts of:

identifying first regular spatial patterns in the first spatial-expression pattern
signal;

identifying second regular spatial patterns in the second spatial-expression
pattern signal; and

10       comparing the first and second regular spatial patterns.

80. (Original)  A computer program product as set forth in claim 78, further comprising
acts of:

comparing all formed spatial-expression pattern signals.

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81. (Previously Presented)  A computer program product as set forth in claim 80,
wherein:

the means for comparing all formed spatial-expression pattern signals
involves clustering all formed spatial-expression pattern signals.

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